INFORMATION DISCLOSURE STATEMENT BY APPLICANT				Complete if Known	
				Application Number	New Application 10/564823
				Filing Date	January 18, 2006
				First Named Inventor	STEIN et al
				Group Art Unit	
				Examiner Name	
				Confirmation No.	
Sheet	1	of	1	Attorney Docket Number	2958-135

NON PATENT LITERATURE DOCUMENTS			
Examiner Initials*	Cite No.[1]	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published	T[2]
/MH/	1.	Database EMBL 28 April 2003, INTERNATIONAL HUMAN GENOME SEQUENCING CONSORTIUM, "The DNA sequence of Homo sapiens: similar to expressed squence".	
	2.	Database Geneseq Online, 25 February 2003, "Human liver single exon probe, SEQ ID NO 20133.	
	3.	Database Geneseq Online, 2 August 2002, "Human colon cancer related nucleotide sequence SEQ ID NO: 2340.	
	4.	Otsuka et al., "Differential expression of the L-plastin gene in human colorectal cancer progression and metastasis", BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 289, 2001, pgs. 876-881.	
	5.	Brett et al., "A rapid bioinformatic method identifies novel genes with direct clinical relevance to colon cancer", ONCOGENE, Vol. 20, no. 33, 27 July 2001, pgs. 4581-4585.	
	6.	Knoesel et al., "Incidence of chromosomal imbalances in advanced colorectal carcinomas and their metastases", VIRCHOWS ARCHIV, vol. 440, no. 2, February 2002, pgs. 187-194.	
↓	7.	Database UniProt., Online, 1 October 2003, Schwabe et al, "Putative binding protein 7a5".	

Examiner Signature	/Mark Halvorson/	Date Considered	11/08/2007

*EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.
[1]Unique citation designation number. [2]Applicant is to place a check mark here if English language Translation is attached.

<!--StartFragment-->RESULT 13
ABQ58645
ID ABQ58645 standard; cDNA; 598 BP.
XX
AC ABQ58645;
XX
DT 02-AUG-2002 (first entry)
XX
DE Human colon cancer related nucleotide sequence SEQ ID NO:2340.
XX
KW Human; colon cancer; cancer; tissue profiling; forensic; mapping;
KW genetic analysis; diagnostic; antisense therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200229086-A2.
XX
PD 11-APR-2002.
XX
PF 02-OCT-2001; 2001WO-US030732.
XX
PR 02-OCT-2000; 2000US-0237271P.
XX
PA (FARB) BAYER CORP.
XX
PI Burgess C, Astle JH, Carroll E, Catino TJ, Dwivedi P, Molino GA;
PI Thiaglingam A, Lewis ME;
XX
DR WPI; 2002-426115/45.
XX
PT New isolated nucleic acid that is differentially expressed in cancer
PT tissues useful for determining the presence of colon cancer in a cell or
PT tissue type, and in antisense therapy.
XX
PS Claim 1; Fig 1; 796pp; English.
XX
CC ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially
CC expressed in cancer tissues. ABB78993 to ABB79004 represent proteins
CC encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
CC used in antisense therapy. An antibody immunoreactive with a polypeptide
CC encoded by (I) is useful for detecting cancer in a patient sample, and
CC for detecting the presence or absence of a polynucleotide encoded by a
CC nucleic acid which hybridises to (I) in a cell. A probe/primer derived
CC from (I) can be used for determining the presence of a nucleic acid which
CC hybridises to (I), and for determining the phenotype of cells in a sample
CC of cells from a patient. (I) is useful for determining the presence of
CC colon cancer in a cell or tissue type, for determining the presence or
CC state of other type of cancer, in antisense therapy, to generate
CC macroarrays on a solid surface, to identify a chromosome on which the
CC corresponding gene resides, and in tissue profiling, forensics, genetic
CC analysis, mapping and diagnostic applications. (I) can be used to raise
CC antibodies, and to screen for peptide analogues and antagonists
XX
SQ Sequence 598 BP; 198 A; 118 C; 108 G; 168 T; 0 U; 6 Other;

  Query Match   16.6%; Score 425.8; DB 6; Length 598;
  Best Local Similarity   98.0%; Pred. No. 3.5e-101;
  Matches 438; Conservative   0; Mismatches   8; Indels   1; Gaps   1;

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Qy          1 ATGCTAATCACTGAAAGAAAACATTTTCGGTCAGGAAGAATTGCACAAAGTATGTCTGAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 ATGCTAATCACTGAAAGAAAACATTTTCGGTCAGGAAGAATTGCACAAAGTATGTCTGAA 197

Qy         61 GCAAATTTGATTGACATGGAAGCTGGAAAACTCTCAAAAAGTTGCAATATTACAGAATGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        198 GCAAATTTGATTGACATGGAAGCTGGAAAACTCTCAAAAAGTTGCAATATTACAGAATGC 257

Qy        121 CAGGACCCAGACTTGCTTCACAATTGGCCGGATGCTTTCACCCTTCGTGGTAATAATGCT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 CAGGACCCAGACTTGCTTCACAATTGGCCGGATGCTTTCACCCTTCGTGGTAATAATGCT 317

Qy        181 TCCAAAGTTGCAAATCCATTCTGGAATCAACTGTCTGCTTCTAACCCATTTTTGGATGAC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 TCCAAAGTTGCAAATCCATTCTGGAATCAACTGTCTGCTTCTAACCCATTTTTGGATGAC 377

Qy        241 ATAACTCAACTAAGAAATAACAGGAAGAGAAATAATATTTCCATCTTAAAGGAAGATCCT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ATAACTCAACTAAGAAATAACAGGAAGAGAAATAATATTTCCATCTTAAAGGAAGATCCT 437

Qy        301 TTTCTTTTCTGTAGAGAAATAGAAAATGGAAATTCTTTTGATTCCTCCGGTGATGAACTT 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        438 TTTCTTTTCTGTAGAGAAATAGAAAATGGAAATTCTTTTGATTCCTCCGGTGATNAACTT 497

Qy        361 GATGTGCATCAGTTACTTAGGCAGACTTCCTCAAGAAATTCTGGAAGATCTAAAAGTGTT 420
              |||| |||||| |||||||||| |||||||||||||||||||| ||||||||||||
Db        498 GATGCGCATCANTTACTTAGGCA-ACTTCCTCAAGAAATTCTGGAANATCTAAAAGTGTT 556

Qy        421 TCAGAACTTCTGGACATTTTAGACGAC 447
              ||| ||||||| ||| |||||||| ||
Db        557 TCANAACTTCTNGACTTTTTAGACNAC 583
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<!--EndFragment-->